



SEQUENCE LISTING

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STEWART, EUGENE L
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<120> METHOD FOR IDENTIFYING A GLUCOCORTICOID
RECEPTOR MODULATOR USING THE STRUCTURE OF A GLUCOCORTICOID
RECEPTOR LIGAND BINDING DOMAIN (TITLE AS AMENDED)

<130> PU4803 US

<140> US 10/600,751
<141> 2003-06-20

<150> US 60/390,610
<151> 2002-06-21

<160> 14

<170> FastSEQ for Windows Version 4.0

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```

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Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
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cta aga gga gga gct act gtg aag gtt tct tct gcg tct tca ccc tca ctg 144
 Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
 35 40 45

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gct gtc gct tct caa tca gac tcc aag cag cga aga ctt ttg gtt gat 192
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 Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
 85 90 95

gtg atg gga aat gac ctg gga ttc cca cag cag ggc caa atc agc ctt 336
 Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
 100 105 110

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Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn			
115	120	125	
ctc aat agg tcg acc agt gtt cca gag aac ccc aag agt tca gca tcc		432	
Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser			
130	135	140	
act gct gtg tct gct gcc ccc aca gag aag gag ttt cca aaa act cac		480	
Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His			
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tct gat gta tct tca gaa cag caa cat ttg aag ggc cag act ggc acc		528	
Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr			
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Asn Gly Gly Asn Val Lys Leu Tyr Thr Asp Gln Ser Thr Phe Asp			
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Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu			
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Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn			
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Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys			
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Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr			
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Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr			
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cct ggg gta att aag caa gag aaa ctg ggc aca gtt tac tgt cag gca		912	
Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala			
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Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser			
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Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met			
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aat aca gca tcc ctt tct caa cag cag gat cag aag cct att ttt aat		1056	
Asn Thr Ala Ser Leu Ser Gln Gln Asp Gln Lys Pro Ile Phe Asn			
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Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro			
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gat gta agc tct cct cca tcc agc tcc tca aca gca aca aca gga cca		1248	
Asp Val Ser Ser Pro Pro Ser Ser Ser Thr Ala Thr Thr Gly Pro			
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Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His			
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tat gga gtc tta act tgt gga agc tgt aaa gtt ttc ttc aaa aga gca		1344	
Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala			
435	440	445	
gtg gaa gga cag cac aat tac cta tgt gct gga agg aat gat tgc atc		1392	
Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile			
450	455	460	
atc gat aaa att cga aga aaa aac tgc cca gca tgc cgc tat cga aaa		1440	
Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Tyr Arg Lys			
465	470	475	480
tgt ctt cag gct gga atg aac ctg gaa gct cga aaa aca aag aaa aaa		1488	
Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys Lys Lys			
485	490	495	
ata aaa gga att cag cag gcc act aca gga gtc tca caa gaa acc tct		1536	
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gaa aat cct ggt aac aaa aca ata gtt cct gca acg tta cca caa ctc		1584	
Glu Asn Pro Gly Asn Lys Thr Ile Val Pro Ala Thr Leu Pro Gln Leu			
515	520	525	
acc cct acc ctg gtg tca ctg ttg gag gtt att gaa cct gaa gtg tta		1632	
Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro Glu Val Leu			
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tat gca gga tat gat agc tct gtt cca gac tca act tgg agg atc atg		1680	
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act acg ctc aac atg tta gga ggg cg ^g caa gtg att gca gca gtg aaa		1728	
Thr Thr Leu Asn Met Leu Gly Gly Arg Gln Val Ile Ala Ala Val Lys			
565	570	575	
tgg gca aag gca ata cca ggt ttc agg aac tta cac ctg gat gac caa		1776	
Trp Ala Lys Ala Ile Pro Gly Phe Arg Asn Leu His Leu Asp Asp Gln			
580	585	590	
atg acc cta ctg cag tac tcc tgg atg ttt ctt atg gca ttt gct ctg		1824	
Met Thr Leu Leu Gln Tyr Ser Trp Met Phe Leu Met Ala Phe Ala Leu			
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610	615	620	

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ctc ttg gat tct atg cat gaa gtg gtt gaa aat ctc ctt aac tat tgc Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu Asn Tyr Cys 725 730 735	2208
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tta gct gaa atc atc acc aat cag ata cca aaa tat tca aat gga aat Leu Ala Glu Ile Ile Thr Asn Gln Ile Pro Lys Tyr Ser Asn Gly Asn 755 760 765	2304
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35 40 45
Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
50 55 60
Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
65 70 75 80
Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
85 90 95
Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
100 105 110
Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Ser Ile Ala Asn
115 120 125
Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser

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Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr		
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Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp		
180	185	190
Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr		
195	200	205
Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu		
210	215	220
Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn		
225	230	235
Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys		
245	250	255
Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr		
260	265	270
Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr		
275	280	285
Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala		
290	295	300
Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser		
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Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met		
325	330	335
Asn Thr Ala Ser Leu Ser Gln Gln Asp Gln Lys Pro Ile Phe Asn		
340	345	350
Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln		
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Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro		
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Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro		
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Asp Val Ser Ser Pro Pro Ser Ser Ser Thr Ala Thr Thr Gly Pro		
405	410	415
Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His		
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Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala		
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Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile		
450	455	460
Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Tyr Arg Lys		
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Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys Lys		
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Ile Lys Gly Ile Gln Gln Ala Thr Thr Gly Val Ser Gln Glu Thr Ser		
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Glu Asn Pro Gly Asn Lys Thr Ile Val Pro Ala Thr Leu Pro Gln Leu		
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Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro Glu Val Leu		
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Tyr Ala Gly Tyr Asp Ser Ser Val Pro Asp Ser Thr Trp Arg Ile Met		
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Thr Thr Leu Asn Met Leu Gly Gly Arg Gln Val Ile Ala Ala Val Lys		
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Trp Ala Lys Ala Ile Pro Gly Phe Arg Asn Leu His Leu Asp Asp Gln		
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Met Thr Leu Leu Gln Tyr Ser Trp Met Phe Leu Met Ala Phe Ala Leu		
595	600	605
Gly Trp Arg Ser Tyr Arg Gln Ser Ser Ala Asn Leu Leu Cys Phe Ala		
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Asp Gln Cys Lys His Met Leu Tyr Val Ser Ser Glu Leu His Arg Leu		

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Gln Val Ser Tyr Glu Glu Tyr Leu Cys Met Lys Thr Leu Leu Leu		
660	665	670
Ser Ser Val Pro Lys Asp Gly Leu Lys Ser Gln Glu Leu Phe Asp Glu		
675	680	685
Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile Val Lys Arg		
690	695	700
Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln Leu Thr Lys		
705	710	715
Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu Asn Tyr Cys		
725	730	735
Phe Gln Thr Phe Leu Asp Lys Thr Met Ser Ile Glu Phe Pro Glu Met		
740	745	750
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cta aga gga gga gct act gtg aag gtt tct gcg tct tca ccc tca ctg		144
Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu		
35	40	45
gct gtc gct tct caa tca gac tcc aag cag cga aga ctt ttg gtt gat		192
Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp		
50	55	60
ttt cca aaa ggc tca gta agc aat gcg cag cag cca gat ctg tcc aaa		240
Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys		
65	70	75
		80
gca gtt tca ctc tca atg gga ctg tat atg gga gag aca gaa aca aaa		288
Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys		
85	90	95
gtg atg gga aat gac ctg gga ttc cca cag cag ggc caa atc agc ctt		336
Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu		
100	105	110
tcc tcg ggg gaa aca gac tta aag ctt ttg gaa gaa agc att gca aac		384
Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn		
115	120	125
ctc aat agg tcg acc agt gtt cca gag aac ccc aag agt tca gca tcc		432
Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser		
130	135	140

act gct gtg tct gct gcc ccc aca gag aag gag ttt cca aaa act cac		480
Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His		
145 150 155 160		
tct gat gta tct tca gaa cag caa cat ttg aag ggc cag act ggc acc		528
Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr		
165 170 175		
aac ggt ggc aat gtg aaa ttg tat acc aca gac caa agc acc ttt gac		576
Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp		
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Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr		
195 200 205		
aat gag agt cct tgg aga tca gac ctg ttg ata gat gaa aac ttt ttg		672
Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu		
210 215 220		
cct tct cct ctg gcg gga gaa gac gat tca ttc ctt ttg gaa gga aac		720
Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn		
225 230 235 240		
tcg aat gag gac tgc aag cct ctc att tta ccg gac act aaa ccc aaa		768
Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys		
245 250 255		
att aag gat aat gga gat ctg gtt ttg tca agc ccc agt aat gta aca		816
Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr		
260 265 270		
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Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr		
275 280 285		
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Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala		
290 295 300		
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Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser		
305 310 315 320		
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Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met		
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gat gta agc tct cct cca tcc agc tcc tca aca gca aca aca gga cca		1248	
Asp Val Ser Ser Pro Pro Ser Ser Ser Thr Ala Thr Thr Gly Pro			
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cct ccc aaa ctc tgc ctg gtg tgc tct gat gaa gct tca gga tgt cat		1296	
Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His			
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Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala			
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gtg gaa gga cag cac aat tac cta tgt gct gga agg aat gat tgc atc		1392	
Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile			
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tgt ctt cag gct gga atg aac ctg gaa gct cga aaa aca aag aaa aaa		1488	
Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys Lys			
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ata aaa gga att cag cag gcc act aca gga gtc tca caa gaa acc tct		1536	
Ile Lys Gly Ile Gln Gln Ala Thr Thr Gly Val Ser Gln Glu Thr Ser			
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gaa aat cct ggt aac aaa aca ata gtt cct gca acg tta cca caa ctc		1584	
Glu Asn Pro Gly Asn Lys Thr Ile Val Pro Ala Thr Leu Pro Gln Leu			
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Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro Glu Val Leu			
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Trp Ala Lys Ala Ile Pro Gly Phe Arg Asn Leu His Leu Asp Asp Gln			
580	585	590	
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Met Thr Leu Leu Gln Tyr Ser Trp Met Ser Leu Met Ala Phe Ala Leu			
595	600	605	
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cct gat ctg att att aat gag cag aga atg act cta ccc tgc atg tac		1920	
Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Thr Leu Pro Cys Met Tyr			
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gac caa tgt aaa cac atg ctg tat gtt tcc tct gag tta cac agg ctt		1968	
Asp Gln Cys Lys His Met Leu Tyr Val Ser Ser Glu Leu His Arg Leu			
645	650	655	

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att aga atg acc tac atc aaa gag cta gga aaa gcc att gtc aag agg Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile Val Lys Arg 690 695 700	2112
gaa gga aac tcc agc cag aac tgg cag cgg ttt tat caa ctg aca aaa Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln Leu Thr Lys 705 710 715 720	2160
ctc ttg gat tct atg cat gaa gtg gtt gaa aat ctc ctt aac tat tgc Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu Asn Tyr Cys 725 730 735	2208
ttc caa aca ttt ttg gat aag acc atg agt att gaa ttc ccc gag atg Phe Gln Thr Phe Leu Asp Lys Thr Met Ser Ile Glu Phe Pro Glu Met 740 745 750	2256
tta gct gaa atc atc acc aat cag ata cca aaa tat tca aat gga aat Leu Ala Glu Ile Ile Thr Asn Gln Ile Pro Lys Tyr Ser Asn Gly Asn 755 760 765	2304
atc aaa aaa ctt ctg ttt cat caa aag tga Ile Lys Lys Leu Leu Phe His Gln Lys *	2334
770 775	

<210> 4
<211> 777
<212> PRT
<213> Homo Sapiens

<400> 4
Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
1 5 10 15
Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
20 25 30
Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
35 40 45
Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
50 55 60
Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
65 70 75 80
Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
85 90 95
Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
100 105 110
Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn
115 120 125
Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
130 135 140
Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
145 150 155 160
Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr
165 170 175
Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp
180 185 190

Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr
 195 200 205
 Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu
 210 215 220
 Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn
 225 230 235 240
 Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys
 245 250 255
 Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr
 260 265 270
 Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr
 275 280 285
 Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala
 290 295 300
 Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser
 305 310 315 320
 Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met
 325 330 335
 Asn Thr Ala Ser Leu Ser Gln Gln Asp Gln Lys Pro Ile Phe Asn
 340 345 350
 Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln
 355 360 365
 Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro
 370 375 380
 Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro
 385 390 395 400
 Asp Val Ser Ser Pro Pro Ser Ser Ser Thr Ala Thr Thr Gly Pro
 405 410 415
 Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His
 420 425 430
 Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala
 435 440 445
 Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile
 450 455 460
 Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Tyr Arg Lys
 465 470 475 480
 Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys Lys
 485 490 495
 Ile Lys Gly Ile Gln Gln Ala Thr Thr Gly Val Ser Gln Glu Thr Ser
 500 505 510
 Glu Asn Pro Gly Asn Lys Thr Ile Val Pro Ala Thr Leu Pro Gln Leu
 515 520 525
 Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro Glu Val Leu
 530 535 540
 Tyr Ala Gly Tyr Asp Ser Ser Val Pro Asp Ser Thr Trp Arg Ile Met
 545 550 555 560
 Thr Thr Leu Asn Met Leu Gly Gly Arg Gln Val Ile Ala Ala Val Lys
 565 570 575
 Trp Ala Lys Ala Ile Pro Gly Phe Arg Asn Leu His Leu Asp Asp Gln
 580 585 590
 Met Thr Leu Leu Gln Tyr Ser Trp Met Ser Leu Met Ala Phe Ala Leu
 595 600 605
 Gly Trp Arg Ser Tyr Arg Gln Ser Ser Ala Asn Leu Leu Cys Phe Ala
 610 615 620
 Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Thr Leu Pro Cys Met Tyr
 625 630 635 640
 Asp Gln Cys Lys His Met Leu Tyr Val Ser Ser Glu Leu His Arg Leu
 645 650 655
 Gln Val Ser Tyr Glu Glu Tyr Leu Cys Met Lys Thr Leu Leu Leu
 660 665 670
 Ser Ser Val Pro Lys Asp Gly Leu Lys Ser Gln Glu Leu Phe Asp Glu
 675 680 685
 Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile Val Lys Arg
 690 695 700

Glu	Gly	Asn	Ser	Ser	Gln	Asn	Trp	Gln	Arg	Phe	Tyr	Gln	Leu	Thr	Lys
705					710				715				720		
Leu	Leu	Asp	Ser	Met	His	Glu	Val	Val	Glu	Asn	Leu	Leu	Asn	Tyr	Cys
				725					730				735		
Phe	Gln	Thr	Phe	Leu	Asp	Lys	Thr	Met	Ser	Ile	Glu	Phe	Pro	Glu	Met
				740				745				750			
Leu	Ala	Glu	Ile	Ile	Thr	Asn	Gln	Ile	Pro	Lys	Tyr	Ser	Asn	Gly	Asn
				755				760				765			
Ile	Lys	Lys	Leu	Leu	Phe	His	Gln	Lys							
				770				775							

<210> 5
<211> 774
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(774)

<400> 5																
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Val	Pro	Ala	Thr	Leu	Pro	Gln	Leu	Thr	Pro	Thr	Leu	Val	Ser	Leu	Leu	
1				5					10				15			
gag	gtt	att	gaa	cct	gaa	gtg	tta	tat	gca	gga	tat	gat	agc	tct	gtt	96
Glu	Val	Ile	Glu	Pro	Glu	Val	Leu	Tyr	Ala	Gly	Tyr	Asp	Ser	Ser	Val	
								20		25			30			
cca	gac	tca	act	tgg	agg	atc	atg	act	acg	ctc	aac	atg	tta	gga	ggg	144
Pro	Asp	Ser	Thr	Trp	Arg	Ile	Met	Thr	Thr	Leu	Asn	Met	Leu	Gly	Gly	
							35		40			45				
cg	caa	gtg	att	gca	gca	gtg	aaa	tgg	gca	aag	gca	ata	cca	ggt	ttc	192
Arg	Gln	Val	Ile	Ala	Ala	Val	Lys	Trp	Ala	Lys	Ala	Ile	Pro	Gly	Phe	
							50		55			60				
agg	aac	tta	cac	ctg	gat	gac	caa	atg	acc	cta	ctg	cag	tac	tcc	tgg	240
Arg	Asn	Leu	His	Leu	Asp	Asp	Gln	Met	Thr	Leu	Leu	Gln	Tyr	Ser	Trp	
							65		70			75		80		
atg	ttt	ctt	atg	gca	ttt	gct	ctg	ggg	tgg	aga	tca	tat	aga	caa	tca	288
Met	Phe	Leu	Met	Ala	Phe	Ala	Leu	Gly	Trp	Arg	Ser	Tyr	Arg	Gln	Ser	
							85		90			95				
agt	gca	aac	ctg	ctg	tgt	ttt	gct	cct	gat	ctg	att	att	aat	gag	cag	336
Ser	Ala	Asn	Leu	Leu	Cys	Phe	Ala	Pro	Asp	Leu	Ile	Ile	Asn	Glu	Gln	
							100		105			110				
aga	atg	act	cta	ccc	tgc	atg	tac	gac	caa	tgt	aaa	cac	atg	ctg	tat	384
Arg	Met	Thr	Leu	Pro	Cys	Met	Tyr	Asp	Gln	Cys	Lys	His	Met	Leu	Tyr	
							115		120			125				
gtt	tcc	tct	gag	tta	cac	agg	ctt	cag	gta	tct	tat	gaa	gag	tat	ctc	432
Val	Ser	Ser	Glu	Leu	His	Arg	Leu	Gln	Val	Ser	Tyr	Glu	Glu	Tyr	Leu	
							130		135			140				
tgt	atg	aaa	acc	tta	ctg	ctt	ctc	tct	tca	gtt	cct	aag	gac	ggt	ctg	480
Cys	Met	Lys	Thr	Leu	Leu	Leu	Leu	Ser	Ser	Val	Pro	Lys	Asp	Gly	Leu	
								145		150		155		160		
aag	agc	caa	gag	cta	ttt	gat	gaa	att	aga	atg	acc	tac	atc	aaa	gag	528
Lys	Ser	Gln	Glu	Leu	Phe	Asp	Glu	Ile	Arg	Met	Thr	Tyr	Ile	Lys	Glu	

165	170	175	
cta gga aaa gcc att gtc aag agg gaa gga aac tcc agc cag aac tgg Leu Gly Lys Ala Ile Val Lys Arg Glu Gly Asn Ser Ser Gln Asn Trp 180	185	190	576
cag cggtt tat caa ctg aca aaa ctc ttg gat tct atg cat gaa gtg Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Met His Glu Val 195	200	205	624
gtt gaa aat ctc ctt aac tat tgc ttc caa aca ttt ttg gat aag acc Val Glu Asn Leu Leu Asn Tyr Cys Phe Gln Thr Phe Leu Asp Lys Thr 210	215	220	672
atg agt att gaa ttc ccc gag atg tta gct gaa atc atc acc aat cag Met Ser Ile Glu Phe Pro Glu Met Leu Ala Glu Ile Ile Thr Asn Gln 225	230	235	720
ata cca aaa tat tca aat gga aat atc aaa aaa ctt ctg ttt cat caa Ile Pro Lys Tyr Ser Asn Gly Asn Ile Lys Lys Leu Leu Phe His Gln 245	250	255	768
aag tga Lys *			774

<210> 6
<211> 257
<212> PRT
<213> Homo sapiens

<400> 6
Val Pro Ala Thr Leu Pro Gln Leu Thr Pro Thr Leu Val Ser Leu Leu
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Glu Val Ile Glu Pro Glu Val Leu Tyr Ala Gly Tyr Asp Ser Ser Val
20 25 30
Pro Asp Ser Thr Trp Arg Ile Met Thr Thr Leu Asn Met Leu Gly Gly
35 40 45
Arg Gln Val Ile Ala Ala Val Lys Trp Ala Lys Ala Ile Pro Gly Phe
50 55 60
Arg Asn Leu His Leu Asp Asp Gln Met Thr Leu Leu Gln Tyr Ser Trp
65 70 75 80
Met Phe Leu Met Ala Phe Ala Leu Gly Trp Arg Ser Tyr Arg Gln Ser
85 90 95
Ser Ala Asn Leu Leu Cys Phe Ala Pro Asp Leu Ile Ile Asn Glu Gln
100 105 110
Arg Met Thr Leu Pro Cys Met Tyr Asp Gln Cys Lys His Met Leu Tyr
115 120 125
Val Ser Ser Glu Leu His Arg Leu Gln Val Ser Tyr Glu Glu Tyr Leu
130 135 140
Cys Met Lys Thr Leu Leu Leu Ser Ser Val Pro Lys Asp Gly Leu
145 150 155 160
Lys Ser Gln Glu Leu Phe Asp Glu Ile Arg Met Thr Tyr Ile Lys Glu
165 170 175
Leu Gly Lys Ala Ile Val Lys Arg Glu Gly Asn Ser Ser Gln Asn Trp
180 185 190
Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Met His Glu Val
195 200 205
Val Glu Asn Leu Leu Asn Tyr Cys Phe Gln Thr Phe Leu Asp Lys Thr
210 215 220
Met Ser Ile Glu Phe Pro Glu Met Leu Ala Glu Ile Ile Thr Asn Gln
225 230 235 240
Ile Pro Lys Tyr Ser Asn Gly Asn Ile Lys Lys Leu Leu Phe His Gln

245	250	255
Lys		
<210> 7		
<211> 774		
<212> DNA		
<213> Homo sapiens		
<220>		
<221> CDS		
<222> (1)...(774)		
<400> 7		
gtt cct gca acg tta cca caa ctc acc cct acc ctg gtg tca ctg ttg	48	
Val Pro Ala Thr Leu Pro Gln Leu Thr Pro Thr Leu Val Ser Leu Leu		
1 5 10 15		
gag gtt att gaa cct gaa gtg tta tat gca gga tat gat agc tct gtt	96	
Glu Val Ile Glu Pro Glu Val Leu Tyr Ala Gly Tyr Asp Ser Ser Val		
20 25 30		
cca gac tca act tgg agg atc atg act acg ctc aac atg tta gga ggg	144	
Pro Asp Ser Thr Trp Arg Ile Met Thr Thr Leu Asn Met Leu Gly Gly		
35 40 45		
cg ^g c ^a g ^t g ^t a ^t t ^t g ^c a ^c g ^t g ^t a ^{aa} t ^{gg} g ^c a ^a g ^g g ^c a ^t a ^t t ^{tt} g ^c a ^{tt} g ^{tt} t ^{cc} g ^{gg}	192	
Arg Gln Val Ile Ala Ala Val Lys Trp Ala Lys Ala Ile Pro Gly Phe		
50 55 60		
agg aac tta cac ctg gat gac caa atg acc cta ctg cag tac tcc tgg	240	
Arg Asn Leu His Leu Asp Asp Gln Met Thr Leu Leu Gln Tyr Ser Trp		
65 70 75 80		
atg tcc ctt atg gca ttt gct ctg ggg tgg aga tca tat aga caa tca	288	
Met Ser Leu Met Ala Phe Ala Leu Gly Trp Arg Ser Tyr Arg Gln Ser		
85 90 95		
agt gca aac ctg ctg tgt ttt gct cct gat ctg att att aat gag cag	336	
Ser Ala Asn Leu Leu Cys Phe Ala Pro Asp Leu Ile Ile Asn Glu Gln		
100 105 110		
aga atg act cta ccc tgc atg tac gac caa tgt aaa cac atg ctg tat	384	
Arg Met Thr Leu Pro Cys Met Tyr Asp Gln Cys Lys His Met Leu Tyr		
115 120 125		
gtt tcc tct gag tta cac agg ctt cag gta tct tat gaa gag tat ctc	432	
Val Ser Ser Glu Leu His Arg Leu Gln Val Ser Tyr Glu Glu Tyr Leu		
130 135 140		
tgt atg aaa acc tta ctg ctt ctc tct tca gtt cct aag gac ggt ctg	480	
Cys Met Lys Thr Leu Leu Leu Ser Ser Val Pro Lys Asp Gly Leu		
145 150 155 160		
aag agc caa gag cta ttt gat gaa att aga atg acc tac atc aaa gag	528	
Lys Ser Gln Glu Leu Phe Asp Glu Ile Arg Met Thr Tyr Ile Lys Glu		
165 170 175		
cta gga aaa gcc att gtc aag agg gaa gga aac tcc agc cag aac tgg	576	
Leu Gly Lys Ala Ile Val Lys Arg Glu Gly Asn Ser Ser Gln Asn Trp		
180 185 190		
cag cgg ttt tat caa ctg aca aaa ctc ttg gat tct atg cat gaa gtg	624	

<210> 8
<211> 257
<212> PRT
<213> *Homo sapiens*

<400> 8
 Val Pro Ala Thr Leu Pro Gln Leu Thr Pro Thr Leu Val Ser Leu Leu
 1 5 10 15
 Glu Val Ile Glu Pro Glu Val Leu Tyr Ala Gly Tyr Asp Ser Ser Val
 20 25 30
 Pro Asp Ser Thr Trp Arg Ile Met Thr Thr Leu Asn Met Leu Gly Gly
 35 40 45
 Arg Gln Val Ile Ala Ala Val Lys Trp Ala Lys Ala Ile Pro Gly Phe
 50 55 60
 Arg Asn Leu His Leu Asp Asp Gln Met Thr Leu Leu Gln Tyr Ser Trp
 65 70 75 80
 Met Ser Leu Met Ala Phe Ala Leu Gly Trp Arg Ser Tyr Arg Gln Ser
 85 90 95
 Ser Ala Asn Leu Leu Cys Phe Ala Pro Asp Leu Ile Ile Asn Glu Gln
 100 105 110
 Arg Met Thr Leu Pro Cys Met Tyr Asp Gln Cys Lys His Met Leu Tyr
 115 120 125
 Val Ser Ser Glu Leu His Arg Leu Gln Val Ser Tyr Glu Glu Tyr Leu
 130 135 140
 Cys Met Lys Thr Leu Leu Leu Ser Ser Val Pro Lys Asp Gly Leu
 145 150 155 160
 Lys Ser Gln Glu Leu Phe Asp Glu Ile Arg Met Thr Tyr Ile Lys Glu
 165 170 175
 Leu Gly Lys Ala Ile Val Lys Arg Glu Gly Asn Ser Ser Gln Asn Trp
 180 185 190
 Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Met His Glu Val
 195 200 205
 Val Glu Asn Leu Leu Asn Tyr Cys Phe Gln Thr Phe Leu Asp Lys Thr
 210 215 220
 Met Ser Ile Glu Phe Pro Glu Met Leu Ala Glu Ile Ile Thr Asn Gln
 225 230 235 240
 Ile Pro Lys Tyr Ser Asn Gly Asn Ile Lys Lys Leu Leu Phe His Gln
 245 250 255
 Lys

<210> 9
<211> 14

<212> PRT
<213> Homo sapiens

<400> 9
Lys Glu Asn Ala Leu Leu Arg Tyr Leu Leu Asp Lys Asp Asp
1 5 10

<210> 10
<211> 5
<212> PRT
<213> Homo sapeins

<220>
<221> VARIANT
<222> (1)...(5)
<223> Xaa = Any Amino Acid

<400> 10
Leu Xaa Xaa Leu Leu
1 5

<210> 11
<211> 6
<212> PRT
<213> Homo sapiens

<400> 11
Leu Leu Arg Tyr Leu Leu
1 5

<210> 12
<211> 252
<212> PRT
<213> Homo sapiens

<400> 12
Ala Leu Thr Pro Ser Pro Val Met Val Leu Glu Asn Ile Glu Pro Glu
1 5 10 15
Ile Val Tyr Ala Gly Tyr Asp Ser Ser Lys Pro Asp Thr Ala Glu Asn
20 25 30
Leu Leu Ser Thr Leu Asn Arg Leu Ala Gly Lys Gln Met Ile Gln Val
35 40 45
Val Lys Trp Ala Lys Val Leu Pro Gly Phe Lys Asn Leu Pro Leu Glu
50 55 60
Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Cys Leu Ser Ser Phe
65 70 75 80
Ala Leu Ser Trp Arg Ser Tyr Lys His Thr Asn Ser Gln Phe Leu Tyr
85 90 95
Phe Ala Pro Asp Leu Val Phe Asn Glu Glu Lys Met His Gln Ser Ala
100 105 110
Met Tyr Glu Leu Cys Gln Gly Met His Gln Ile Ser Leu Gln Phe Val
115 120 125
Arg Leu Gln Leu Thr Phe Glu Glu Tyr Thr Ile Met Lys Val Leu Leu
130 135 140
Leu Leu Ser Thr Ile Pro Lys Asp Gly Leu Lys Ser Gln Ala Ala Phe
145 150 155 160
Glu Glu Met Arg Thr Asn Tyr Ile Lys Glu Leu Arg Lys Met Val Thr
165 170 175
Lys Cys Pro Asn Asn Ser Gly Gln Ser Trp Gln Arg Phe Tyr Gln Leu
180 185 190
Thr Lys Leu Leu Asp Ser Met His Asp Leu Val Ser Asp Leu Leu Glu

195	200	205
Phe Cys Phe Tyr Thr Phe Arg Glu Ser His Ala Leu Lys Val Glu Phe		
210	215	220
Pro Ala Met Leu Val Glu Ile Ile Ser Asp Gln Leu Pro Lys Val Glu		
225	230	235
Ser Gly Asn Ala Lys Pro Leu Tyr Phe His Arg Lys		
245	250	

<210> 13
<211> 252
<212> PRT
<213> Homo sapiens

<400> 13			
Gln Leu Ile Pro Pro Leu Ile Asn Leu Leu Met Ser Ile Glu Pro Asp			
1	5	10	15
Val Ile Tyr Ala Gly His Asp Asn Thr Lys Pro Asp Thr Ser Ser Ser			
20	25	30	
Leu Leu Thr Ser Leu Asn Gln Leu Gly Glu Arg Gln Leu Leu Ser Val			
35	40	45	
Val Lys Trp Ser Lys Ser Leu Pro Gly Phe Arg Asn Leu His Ile Asp			
50	55	60	
Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser Leu Met Val Phe			
65	70	75	80
Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly Gln Met Leu Tyr			
85	90	95	
Phe Ala Pro Asp Leu Ile Leu Asn Glu Gln Arg Met Lys Glu Ser Ser			
100	105	110	
Phe Tyr Ser Leu Cys Leu Thr Met Trp Gln Ile Pro Gln Glu Phe Val			
115	120	125	
Lys Leu Gln Val Ser Gln Glu Glu Phe Leu Cys Met Lys Val Leu Leu			
130	135	140	
Leu Leu Asn Thr Ile Pro Leu Glu Gly Leu Arg Ser Gln Thr Gln Phe			
145	150	155	160
Glu Glu Met Arg Ser Ser Tyr Ile Arg Glu Leu Ile Lys Ala Ile Gly			
165	170	175	
Leu Arg Gln Lys Gly Val Val Ser Ser Gln Arg Phe Tyr Gln Leu			
180	185	190	
Thr Lys Leu Asp Asn Leu His Asp Leu Val Lys Gln Leu His Leu			
195	200	205	
Tyr Cys Leu Asn Thr Phe Ile Gln Ser Arg Ala Leu Ser Val Glu Phe			
210	215	220	
Pro Glu Met Met Ser Glu Val Ile Ala Ala Gln Leu Pro Lys Ile Leu			
225	230	235	240
Ala Gly Met Val Lys Pro Leu Leu Phe His Lys Lys			
245	250		

<210> 14
<211> 252
<212> PRT
<213> Homo sapiens

<400> 14			
Glu Cys Gln Pro Ile Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly			
1	5	10	15
Val Val Cys Ala Gly His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala			
20	25	30	
Leu Leu Ser Ser Leu Asn Glu Leu Gly Glu Arg Gln Leu Val His Val			
35	40	45	
Val Lys Trp Ala Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp			
50	55	60	
Asp Gln Met Ala Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe			

65	70	75	80
Ala Met Gly Trp Arg Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr			
85	90	95	
Phe Ala Pro Asp Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg			
100	105	110	
Met Tyr Ser Gln Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly			
115	120	125	
Trp Leu Gln Ile Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu			
130	135	140	
Leu Phe Ser Ile Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe			
145	150	155	160
Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala			
165	170	175	
Cys Lys Arg Lys Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu			
180	185	190	
Thr Lys Leu Leu Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln			
195	200	205	
Phe Thr Phe Asp Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe			
210	215	220	
Pro Glu Met Met Ala Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu			
225	230	235	240
Ser Gly Lys Val Lys Pro Ile Tyr Phe His Thr Gln			
245	250		